#2   OIPE

RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/10/011,859   TIME: 09:36:57

Input Set : N:\Crf3\RULE60\10011859.raw   ENTERED
Output Set: N:\CRF3\02062002\J011859.raw

```
  1 <110> APPLICANT: Sheppard, Paul O.
  2        Jaspers, Stephen R.
  3 <120> TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS
  4 <130> FILE REFERENCE: 97-75
  5 <140> CURRENT APPLICATION NUMBER: 10/011,859
  6 <141> CURRENT FILING DATE: 2001-11-05
  8 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/253,316
W--> 9 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-19
 11 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/075,300
W-->12 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-20
 13 <160> NUMBER OF SEQ ID NOS: 34
 14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1142
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (17)...(1078)
 23 <400> SEQUENCE: 1.
 24     ccacggtccc agcgac atg cag ggg ctc ctc ttc ccc act ctt ctg ctt gct    52
 25                    Met Gln Gly Leu Leu Phe Pro Thr Leu Leu Leu Ala
 26                     1           5                   10
 27     ggc ctg gca cag ttc tgc tgc agg gta cag ggc act gga cca tta gat    100
 28     Gly Leu Ala Gln Phe Cys Cys Arg Val Gln Gly Thr Gly Pro Leu Asp
 29              15                  20                  25
 30     aca aca cct gaa gga agg cct gga gaa gtg tca gat gca cct cag cgt    148
 31     Thr Thr Pro Glu Gly Arg Pro Gly Glu Val Ser Asp Ala Pro Gln Arg
 32          30                  35                  40
 33     aaa cag ttt tgt cac tgg ccc tgc aaa tgc cct cag cag aag ccc cgt    196
 34     Lys Gln Phe Cys His Trp Pro Cys Lys Cys Pro Gln Gln Lys Pro Arg
 35      45              50                  55                  60
 36     tgc cct cct gga gtg agc ctg gtg aga gat ggc tgt gga tgc tgt aaa    244
 37     Cys Pro Pro Gly Val Ser Leu Val Arg Asp Gly Cys Gly Cys Cys Lys
 38                  65                  70                  75
 39     atc tgt gcc aag caa cca ggg gaa atc tgc aat gaa gct gac ctc tgt    292
 40     Ile Cys Ala Lys Gln Pro Gly Glu Ile Cys Asn Glu Ala Asp Leu Cys
 41              80                  85                  90
 42     gac cca cac aaa ggg ctg tat tgt gac tac tca gta gac agg cct agg    340
 43     Asp Pro His Lys Gly Leu Tyr Cys Asp Tyr Ser Val Asp Arg Pro Arg
 44              95                  100                 105
 45     tac gag act gga gtg tgt gca tac ctt gta gct gtt ggg tgc gag ttc    388
 46     Tyr Glu Thr Gly Val Cys Ala Tyr Leu Val Ala Val Gly Cys Glu Phe
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```
47            110                115                120
48      aac cag gta cat tat cat aat ggc caa gtg ttt cag ccc aac ccc ttg      436
49      Asn Gln Val His Tyr His Asn Gly Gln Val Phe Gln Pro Asn Pro Leu
50      125                130                135                140
51      ttc agc tgc ctc tgt gtg agt ggg gcc att gga tgc aca cct ctg ttc      484
52      Phe Ser Cys Leu Cys Val Ser Gly Ala Ile Gly Cys Thr Pro Leu Phe
53                        145                150                155
54      ata cca aag ctg gct ggc agt cac tgc tct gga gct aaa ggt gga aag      532
55      Ile Pro Lys Leu Ala Gly Ser His Cys Ser Gly Ala Lys Gly Gly Lys
56                        160                165                170
57      aag tct gat cag tca aac tgt agc ctg gaa cca tta cta cag cag ctt      580
58      Lys Ser Asp Gln Ser Asn Cys Ser Leu Glu Pro Leu Leu Gln Gln Leu
59                175                180                185
60      tca aca agc tac aaa aca atg cca gct tat aga aat ctc cca ctt att      628
61      Ser Thr Ser Tyr Lys Thr Met Pro Ala Tyr Arg Asn Leu Pro Leu Ile
62            190                195                200
63      tgg aaa aaa aaa tgt ctt gtg caa gca aca aaa tgg act ccc tgc tcc      676
64      Trp Lys Lys Lys Cys Leu Val Gln Ala Thr Lys Trp Thr Pro Cys Ser
65      205                210                215                220
66      aga aca tgt ggg atg gga ata tct aac agg gtg acc aat gaa aac agc      724
67      Arg Thr Cys Gly Met Gly Ile Ser Asn Arg Val Thr Asn Glu Asn Ser
68                        225                230                235
69      aac tgt gaa atg aga aaa gag aaa aga ctg tgt tac att cag cct tgc      772
70      Asn Cys Glu Met Arg Lys Glu Lys Arg Leu Cys Tyr Ile Gln Pro Cys
71                        240                245                250
72      gac agc aat ata tta aag aca ata aag att ccc aaa gga aaa aca tgc      820
73      Asp Ser Asn Ile Leu Lys Thr Ile Lys Ile Pro Lys Gly Lys Thr Cys
74                        255                260                265
75      caa cct act ttc caa ctc tcc aaa gct gaa aaa ttt gtc ttt tct gga      868
76      Gln Pro Thr Phe Gln Leu Ser Lys Ala Glu Lys Phe Val Phe Ser Gly
77                270                275                280
78      tgc tca agt act cag agt tac aaa ccc act ttt tgt gga ata tgc ttg      916
79      Cys Ser Ser Thr Gln Ser Tyr Lys Pro Thr Phe Cys Gly Ile Cys Leu
80      285                290                295                300
81      gat aag aga tgc tgt atc cct aat aag tct aaa atg att act att caa      964
82      Asp Lys Arg Cys Cys Ile Pro Asn Lys Ser Lys Met Ile Thr Ile Gln
83                        305                310                315
84      ttt gat tgc cca aat gag ggg tca ttt aaa tgg aag atg ctg tgg att      1012
85      Phe Asp Cys Pro Asn Glu Gly Ser Phe Lys Trp Lys Met Leu Trp Ile
86                        320                325                330
87      aca tct tgt gtg tgt cag aga aac tgc aga gaa cct gga gat ata ttt      1060
88      Thr Ser Cys Val Cys Gln Arg Asn Cys Arg Glu Pro Gly Asp Ile Phe
89                335                340                345
90      tct gag ctc aag att ctg taaaaccaag caaatggggg aaaagttagt      1108
91      Ser Glu Leu Lys Ile Leu
92            350
93      caatcctgtc atataataaa aaaattagtg agta      1142
95  <210> SEQ ID NO: 2
96  <211> LENGTH: 354
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97  <212> TYPE: PRT
98  <213> ORGANISM: Homo sapiens
99  <400> SEQUENCE: 2
100       Met Gln Gly Leu Leu Phe Pro Thr Leu Leu Leu Ala Gly Leu Ala Gln
101       1                   5                   10                  15
102       Phe Cys Cys Arg Val Gln Gly Thr Gly Pro Leu Asp Thr Thr Pro Glu
103                   20                  25                  30
104       Gly Arg Pro Gly Glu Val Ser Asp Ala Pro Gln Arg Lys Gln Phe Cys
105            :     35              40                  45
106       His Trp Pro Cys Lys Cys Pro Gln Gln Lys Pro Arg Cys Pro Pro Gly
107            50                  55                  60
108       Val Ser Leu Val Arg Asp Gly Cys Gly Cys Cys Lys Ile Cys Ala Lys
109       65                  70                  75                  80
110       Gln Pro Gly Glu Ile Cys Asn Glu Ala Asp Leu Cys Asp Pro His Lys
111                   85                  90                  95
112       Gly Leu Tyr Cys Asp Tyr Ser Val Asp Arg Pro Arg Tyr Glu Thr Gly
113                   100                 105                 110
114       Val Cys Ala Tyr Leu Val Ala Val Gly Cys Glu Phe Asn Gln Val His
115                   115                 120                 125
116       Tyr His Asn Gly Gln Val Phe Gln Pro Asn Pro Leu Phe Ser Cys Leu
117            130                 135                 140
118       Cys Val Ser Gly Ala Ile Gly Cys Thr Pro Leu Phe Ile Pro Lys Leu
119       145                 150                 155                 160
120       Ala Gly Ser His Cys Ser Gly Ala Lys Gly Gly Lys Lys Ser Asp Gln
121                   165                 170                 175
122       Ser Asn Cys Ser Leu Glu Pro Leu Leu Gln Gln Leu Ser Thr Ser Tyr
123                   180                 185                 190
124       Lys Thr Met Pro Ala Tyr Arg Asn Leu Pro Leu Ile Trp Lys Lys Lys
125            195                 200                 205
126       Cys Leu Val Gln Ala Thr Lys Trp Thr Pro Cys Ser Arg Thr Cys Gly
127            210                 215                 220
128       Met Gly Ile Ser Asn Arg Val Thr Asn Glu Asn Ser Asn Cys Glu Met
129       225                 230                 235                 240
130       Arg Lys Glu Lys Arg Leu Cys Tyr Ile Gln Pro Cys Asp Ser Asn Ile
131                   245                 250                 255
132       Leu Lys Thr Ile Lys Ile Pro Lys Gly Lys Thr Cys Gln Pro Thr Phe
133                   260                 265                 270
134       Gln Leu Ser Lys Ala Glu Lys Phe Val Phe Ser Gly Cys Ser Ser Thr
135                   275                 280                 285
136       Gln Ser Tyr Lys Pro Thr Phe Cys Gly Ile Cys Leu Asp Lys Arg Cys
137            290                 295                 300
138       Cys Ile Pro Asn Lys Ser Lys Met Ile Thr Ile Gln Phe Asp Cys Pro
139       305                 310                 315                 320
140       Asn Glu Gly Ser Phe Lys Trp Lys Met Leu Trp Ile Thr Ser Cys Val
141                   325                 330                 335
142       Cys Gln Arg Asn Cys Arg Glu Pro Gly Asp Ile Phe Ser Glu Leu Lys
143            340                 345                 350
144       Ile Leu
146  <210> SEQ ID NO: 3
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RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/10/011,859   TIME: 09:36:57

Input Set : N:\Crf3\RULE60\10011859.raw
Output Set: N:\CRF3\02062002\J011859.raw

```
      147 <211> LENGTH: 1062
      148 <212> TYPE: DNA
      149 <213> ORGANISM: Artificial Sequence
      150 <220> FEATURE:
      151 <223> OTHER INFORMATION: Degenerate sequence
      152 <220> FEATURE:
      153 <221> NAME/KEY: misc_feature
      154 <222> LOCATION: (1)...(1062)
      155 <223> OTHER INFORMATION: n = A,T,C or G
      156 <400> SEQUENCE: 3
W--> 157        atgcarggny tnytnttycc nacnytnytn ytngcnggny tngcncartt ytgytgymgn        60
W--> 158        gtncarggna cnggnccnyt ngayacnacn ccngarggnm gnccnggnga rgtnwsngay       120
W--> 159        gcnccncarm gnaarcartt ytgycaytgg ccntgyaart gyccncarca raarccnmgn       180
W--> 160        tgyccnccng gngtnwsnyt ngtnmgngay ggntgyggnt gytgyaarat htgygcnaar       240
W--> 161        carccnggng arathtgyaa ygargcngay ytntgygayc cncayaargg nytntaytgy       300
W--> 162        gaytaywsng tngaymgncc nmgntaygar acnggngtnt gygcntayyt ngtngcngtn       360
W--> 163        ggntgygart tyaaycargt ncaytaycay aayggncarg tnttycarcc naayccnytn       420
W--> 164        ttywsntgyy tntgygtnws nggngcnath ggntgyacnc cnytnttyat hccnaarytn       480
W--> 165        gcnggnwsnc aytgywsngg ngcnaarggn ggnaaraarw sngaycarws naaytgywsn       540
W--> 166        ytngarccny tnytncarca rytnwsnacn wsntayaara cnatgccngc ntaymgnaay       600
W--> 167        ytnccnytna thtggaaraa raartgyytn gtncargcna cnaartggac nccntgywsn       660
W--> 168        mgnacntgyg gnatgggnat hwsnaaymgn gtnacnaayg araaywsnaa ytgygaratg       720
W--> 169        mgnaargara armgnytntg ytayathcar ccntgygayw snaayathyt naaracnath       780
W--> 170        aarathccna arggnaarac ntgycarccn acnttycary tnwsnaargc ngaraartty       840
W--> 171        gtnttywsng gntgywsnws nacncarwsn tayaarccna cnttytgygg nathtgyytn       900
W--> 172        gayaarmgnt gytgyathcc naayaarwsn aaratgatha cnathcartt ygaytgyccn       960
W--> 173        aaygarggnw snttyaartg gaaratgytn tggathacnw sntgygtntg ycarmgnaay      1020
W--> 174        tgymgngarc cnggngayat httywsngar ytnaarathy tn                         1062
      176 <210> SEQ ID NO: 4
      177 <211> LENGTH: 279
      178 <212> TYPE: DNA
      179 <213> ORGANISM: Mus musculus
      180 <400> SEQUENCE: 4
      181        atccccagag gagaaacatg tcaacccact ttccaactcc ccaaagctga aaaatttgtt        60
      182        ttttctggat gctcaagcac tcagagttac agacccactt tctgtggaat atgcctggac       120
      183        aagagatgct gtgtccccaa caaatctaaa atgattactg ttaggtttga ctgccccagt       180
      184        gaagggtcat ttaagtggca gatgctgtgg gtcacatctt gtgtgtgtca gagggactgc       240
      185        agagaaccag gagatatatt ttctgagctc aggattcta                               279
      187 <210> SEQ ID NO: 5
      188 <211> LENGTH: 93
      189 <212> TYPE: PRT
      190 <213> ORGANISM: Mus musculus
      191 <400> SEQUENCE: 5
      192        Ile Pro Arg Gly Glu Thr Cys Gln Pro Thr Phe Gln Leu Pro Lys Ala
      193         1               5                  10                  15
      194        Glu Lys Phe Val Phe Ser Gly Cys Ser Ser Thr Gln Ser Tyr Arg Pro
      195                       20                  25                  30
      196        Thr Phe Cys Gly Ile Cys Leu Asp Lys Arg Cys Cys Val Pro Asn Lys
      197                       35                  40                  45
```

```
198        Ser Lys Met Ile Thr Val Arg Phe Asp Cys Pro Ser Glu Gly Ser Phe
199            50                  55                  60
200        Lys Trp Gln Met Leu Trp Val Thr Ser Cys Val Cys Gln Arg Asp Cys
201        65                  70                  75                  80
202        Arg Glu Pro Gly Asp Ile Phe Ser Glu Leu Arg Ile Leu
203                        85                  90
205 <210> SEQ ID NO: 6
206 <211> LENGTH: 22
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: oligonucleotide primer ZC14882
211 <400> SEQUENCE: 6
212        aacttttccc ccatttgctt gg                                    22
214 <210> SEQ ID NO: 7
215 <211> LENGTH: 21
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: oligonucleotide primer ZC14883
220 <400> SEQUENCE: 7
221        acaaaatgga ctccctgctc c                                     21
223 <210> SEQ ID NO: 8
224 <211> LENGTH: 22
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: oligonucleotide primer ZC15909
229 <400> SEQUENCE: 8
230        tcgtccaacg actataaaga gg                                    22
232 <210> SEQ ID NO: 9
233 <211> LENGTH: 21
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: oligonucleotide primer ZC14885
238 <400> SEQUENCE: 9
239        ttgctgtcgc aaggctgaat g                                     21
241 <210> SEQ ID NO: 10
242 <211> LENGTH: 21
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: oligonucleotide primer ZC15911
247 <400> SEQUENCE: 10
248        aggctgtcct ctaagcgtca c                                     21
250 <210> SEQ ID NO: 11
251 <211> LENGTH: 21
252 <212> TYPE: DNA
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VERIFICATION SUMMARY   DATE: 02/06/2002
PATENT APPLICATION: **US/10/011,859**   TIME: 09:36:58

Input Set : **N:\Crf3\RULE60\10011859.raw**
Output Set: **N:\CRF3\02062002\J011859.raw**

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L:9 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:436 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
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